caBIG Meeting Record

Integrative Cancer Research/Microarray Repositories SIG Teleconference
2:00 – 3:00 PM ET
December 1st, 2004

Teleconference Information: (Phone) (Passcode) (Moderator)	USA Toll Free Number: 800-593-0616 Passcode: 4152325 Moderator: Julie Zhu
Net-Centra Information: (URL) (Meeting ID)	
Key Decisions and/or Outcomes: *(copy & paste from agenda)*	▪ Mervi Heiskanen and others on the caArray team gave an update on the caArray user acceptance testing, the status of bug fixes, and on the 1.0 release. ▪ Ari Kahn and David Kane from NCI-CCR gave an update on the NCI-60 data sharing project ▪ Scott Li from TJ-Kimmel gave an overview of the zebrafish data sharing project ▪ Funded centers will take turn to take meeting minutes starting in January 2005
Executive Summary:	This teleconference focused on the status update, existing issues and possible solutions for caArray, NCI-60 and Zebrafish Microarray Repository Projects.
Action Items:	Bullet action items here: ▪ John Moy will set up a ftp site next week for caArray users to download caArray documentation and training guide materials. ▪ Mervi Heiskanen will post updated bug list on UAT or users listserv next week. ▪ Mervi Heiskanen will send to the caArray user list the hardware specification currently used for caArray ▪ Julie Zhu will send the meeting minutes on December 2nd 2004 to the Microarray Repository SIG. ▪ Microarray Repository SIG participants will review the

	meeting minutes and send comments back to Julie Zhu in 2 days. ▪ Scott Li will send the design documentation and use cases of Zebrafish Microarray Repository to Mervi Heiskanen and Juli Klemm before December 3rd 2004. ▪ Julie Zhu will send the Microarray Repository SIG participant list to NCIBC application support to be added to the caArray user listserv next week. ▪ Julie Zhu will send out the rotation list for each funded participating center to take turns to take meeting minutes next week.
Next Steps:	The next teleconference will focus on the status update, existing issues and possible solutions for caArray, NCI-60 and Zebrafish Microarray Repository Projects.
Attendees:	The following were present: ▪ Don Baldwin (University of Pennsylvania) ▪ Bart Brown (University of Iowa) ▪ Leo Cheung (University of Hawaii) ▪ KS Doctor (The Burnham Institute) ▪ Joel Dubbels (IBM) ▪ Steve Enkemann (Moffitt Cancer Center) ▪ Steven Eschrich (Moffitt Cancer Center) ▪ Mervi Heiskanen (National Cancer Institute) ▪ Maureen Higgins (Memorial Sloan Kettering) ▪ Ari Kahn (National Cancer Institute) ▪ David Kane (MCI TCR) ▪ Jamie Keller (NCICB) ▪ Javed Khan (NCI-CCR) ▪ Juli Klemm (BAH) ▪ Gene Kraus (Karmanos Cancer Institute) ▪ Scott Li (Thomas Jefferson University) ▪ Juergen Lorenz (SAIC) ▪ Jomol Mathew (NYU School of Medicine) ▪ Mary McAdams(IMS) ▪ John Moy (NCICB) ▪ John Osborne (Northwestern University) ▪ John Powell (NIH) ▪ Jennifer Shoemaker (Duke University Medical Center) ▪ Louise Showe (Wistar) ▪ Paul Spellman (LBL)

	▪ Don Swan (NCICB) ▪ Taku Tokuyasu (UCSF) ▪ Julie Zhu (Northwestern University)
Detailed Meeting Notes: *(copy & paste from agenda and place your meeting notes under each agenda item)*	**2:00 - 2:05, roll-call, open meeting, review meeting goals (Julie Zhu)** **2:05 - 2:10, review discussion of last meeting (Julie Zhu)** ▪ In the previous teleconference, John Weinstein, Ari Kahn and David Kane gave a presentation on NCI-60 Project and Mervi Heiskanen gave us a status update on caAarray beta release and UAT. ▪ Thanks to Juli Klemm, the slides and the meeting minutes are available to download from the caBIG website. ▪ Juli Klemm and Mervi Heiskanen have set up a caArray developer group to discuss technical issues using caArray API to develop tools interacting with caArray database and application. The caArray developer group just had its first teleconference a couple of hours ago. If you are interested in participating in the caArray developer group, please contact Mervi Heiskanen to be added to the caArray developer listserv. The listserv address is CAARRAY_DEVELOPERS-L@LIST.NIH.GOV. **2:10 - 2:35, update on caArray release and user acceptance testing (Mervi Heiskanen)** ▪ The caArray UAT went very well and a lot of bugs and feedback have been reported to caArray developer team ▪ John Moy explained the bug classification system. Bugs are classified into 4 categories: urgent, high, medium and low priority. Currently, there are 5 urgent, 23 high, 4 medium and 19 low priority bugs. ▪ Mervi Heiskanen pointed out that caArray 1.0 release will be focusing on fixing issues related to functionality defects, caBIG compatibility and MIAME compliant issues. ▪ For the caArray 1.0 release, the urgent and high priority bugs will be fixed. In addition, Eighty-six features have been requested through UAT which will likely be incorporated into caArray 1.2 release. The medium and low priority bugs will be fixed for caArray 1.2 as well. Mervi suggested having a vote on what features people want for version 1.1 in the form of forum. ▪ CaArray 1.0 is scheduled to release on January 31st 2005. It is

tested in Oracle only and the release will include

- Package GUI
- API
- Technical documentation and user guide
- Training Materials
- Known defects and workarounds

- Juli Klemm asked whether there is an upgrade program from beta to 1.0. According to Mervi, there will not be an upgrade program for upgrading beta version to 1.0. Therefore the recommendation for caArray adopters is to wait for the 1.0 release and not install beta version now.
- Scott Li asked where there is more testing of beta going on and whether there is training material available.
  - Mervi suggest send email to NCICB application support to get account to test caArray beta version.
  - Currently there is no online tutorial available. For training, please contact Mervi
- According to John Moy, the following documentations are available and he will set up a ftp site for caArray adopters to download.
  - Javadoc for MAGE-OM API
  - Install me doc
  - Read me doc
  - Known defects,
  - Training guide
  - Quick start guide
  - According to Jamie, quick start guide is Powerpoint presentation and longer training will not be available until end of January
- Mervi explained the caArray listservs and encouraged people to communicate through listserv.
  - UAT list is going to be moved to caArray general user listserv. Julli Klemm pointed out that everybody on this SIG should be in the user listserv
  - Developer list is for people who are developing tools interacting with caArray.

- Julie Zhu will send all the people on this SIG to the NCICB application support to be added in bulk. For people who join the SIG in the future, please send email to NCICB applications support if you want to join the list.

2:35 - 2:40, update on NCI-60 Project (Ari Khan)

- Most of our attention has been focused on completing the Work Plan. In the process we have come to several conclusions and decisions.
- Cell Level Characterization
  - MAGE-OM may satisfy initial characterization
  - Modest extensions may be needed for data such as disputed cell lines. For example, some breast cell lines are now thought to be melanomas although it is still in dispute. We would like to represent this.
    - To represent this sort of data in MAGE-OM, using Biosource to define our own ontology was proposed as a solution in this teleconference.
- Affymetrix MAGE-ML annotation and MAGE-ML production
  - Use a local installation of MIAMExpress
    - Represents MAGE-OM well
    - For data fields that can't be represented in MIAMExpress, we'll add those fields to the MAGE-ML using another method after it has been generated from MIAMExpress instead of reengineering MIAMExpress.
    - We'll use MIAMExpress for cDNA annotation and MAGE-ML production
- Drug Therapeutics Program Datasets
  - We'll use a local installation of tox-MIAMExpress for annotation and XML production.
- Array CGH Data
  - caArray submission requires GenePix format and caArray is going to provide this script to make the conversion for the 1.0 release
- Issues for importing MAGE-ML produced from MIAMExpress to caArray
  - Need to test the import
  - No built-in validation of MAGE-ML in caArray yet

2:40 - 2:50, update on Zebrafish Microarray Repository Project (Scott Li)

	▪ Working on SOW with Juli Klemm ▪ Zebrafish is currently used at Thomas Jefferson as model system to study cardiovascular system and fat metabolism. ▪ Currently the data is housed in MAGGIE system and it captures MIAME information. ▪ The Microarray platform is single-colored in-house printed 60k oligo array. ▪ MAGGIE is virtual directory service for desktop applications. It can be seen as a raw data resources potentially being consumed by desktop annotation tools. We'd like to reuse this resource for zebrafish data annotation and other microarray data annotation. ▪ Looking for the best way to integrate current MAGGIE with caArray **2:50 - 3:00, set agenda for next meeting (All)** ▪ Next meeting will be focusing on status update for all the three projects in this SIG ▪ Regarding taking meeting minutes for the future teleconferences, Juli Klemm suggested rotate around funded centers
Other *(copy & paste from agenda)*	